

What is claimed is:

1. A method of identifying an animal which possesses a genotype indicative of favorable meat quality traits, said
5 method comprising:
 - a) obtaining a nucleic acid sample from said animal,
and
 - b) assaying for the presence of a polymorphism in the
10 MC4R gene of the sample, or a polymorphism linked
thereto, said polymorphism being one which is
associated with favorable meat quality
characteristics such pH, marbling, color and drip
loss.
- 15 2. The method of claim 1 wherein said polymorphism is
characterized by an aspartic acid codon (GAU) which is
changed to an asparagine codon (AAU) at amino acid position
analogous to amino acid 298 of a human MC4R gene product.
- 20 3. The method of claim 1 wherein said aspartic acid codon
at position 298 of the MC4R gene product is associated with
improved meat characteristics.
4. The method of claim 1 wherein the animal is a pig.
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5. The method of claim 1 wherein the step of identifying
the polymorphism is a method employing allele specific
oligonucleotides.
- 30 6. The method of claim 1 wherein said polymorphism is
identified by PCR amplification and restriction.

7. The method of claim 1 wherein the step of identifying the polymorphism is selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), temperature gradient gel electrophoresis (TGGE), and use of linked genetic markers.
8. The method of claim 7 wherein the step of identifying the polymorphism comprises RFLP analysis.
9. The method of claim 1 further comprising the step of: amplifying the MC4R gene sequence.
10. The method of claim 9 further comprising the step of digesting the amplified region with the restriction endonuclease *Taq I*.
11. The amplified gene sequence of claim 10 wherein primers used in the amplification are selected from the group consisting of SEQ. ID NO:6, SEQ. ID NO:7, SEQ. ID NO:8, SEQ. ID NO:9, SEQ. ID NO:10, and SEQ. ID NO:11.
12. A single strand of an oligonucleotide primer useful for detecting nucleotide 678 of SEQ ID NO:1, the primer consisting of a nucleotide sequence having about 4-30 contiguous bases from SEQ ID NO:1 and flanking position 678.
13. The oligonucleotide of claim 12 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:6.
14. The oligonucleotide of claim 12 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:7.

15. The oligonucleotide of claim 12 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:8.

5 16. The oligonucleotide of claim 12 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:9.

10 17. The oligonucleotide of claim 12 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:10.

15 18. The oligonucleotide of claim 12 wherein the oligonucleotide has the nucleotide sequence represented by SEQ ID NO:11.

19. The method of claim 1 wherein said primer is SEQ ID NOS: 6 and 7 and wherein said polymorphism is position 678 of said amplified sequence.

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20. A method of identifying an animal which possess a desired genotype indicative of favorable meat quality characteristics, the method comprising:

- a) obtaining a nucleic acid sample,
- 25 b) digesting the sample with a restriction enzyme that recognizes the same site as *Taq I* to obtain fragments,
- c) separating the fragments obtained from the digestion, and
- 30 d) identifying the presence or absence of a *Taq I* site at the codon for position for the amino acid codon at position 298 of the MC4R gene product.

21. The method of claim 20 further comprising the step of
35 selecting animals with the desired genotype for breeding.

22. The method of claim 20 wherein the site is identifiable by fragments of 466, 225, and 76 bp when a guanine is present at base 678 and fragments of 542 and 225 bp when an adenine is present when a restriction enzyme which cuts at the same recognition site as *Taq I* is used.

23. The method of claim 20 wherein the site is identifiable by fragments of 156 and 70 bp when allele one is present and 226 bp when allele 2 is present, when a restriction enzyme that acts at the same recognition site as *TaqI* is used.

24. The method of claim 20 wherein the step of identifying comprises:
detecting the *Taq I* site by amplification.

25. A kit for evaluating a nucleic acid sample from an animal comprising:
a reagent in a container that identifies a polymorphism in a MC4R gene.

26. The kit of claim 25 wherein the reagent is a primer that amplifies the MC4R gene or a fragment thereof.

27. The kit of claim 25 further comprising:
a DNA polymerase which cleaves the MC4R gene,
a forward primer, and
a reverse primer,
wherein the primers are capable of amplifying a region of the MC4R gene which contains a polymorphic site.

28. A primer for assaying the presence of a polymorphic *TaqI* site in the MC4R gene wherein the primer comprises a sequence selected from the group consisting of SEQ. ID NO:6, SEQ. ID NO:7, SEQ. ID NO:8, SEQ. ID NO:9, SEQ. ID NO:10, and SEQ. ID NO:11.

29. A method for selecting animals for the desired traits of improved meat quality comprising the steps of:

- a) obtaining a nucleic acid sample from an animal,
- b) identifying a polymorphism characterized by a nucleotide position 678 of SEQ ID NO:1 from the MC4R gene, and
- c) selecting the animals which have the nucleotide associated with the desired traits in position 678.

30. A method for an indirect selection for a polymorphism in MC4R wherein specific alleles of an alternative DNA marker are used to make the indirect selection wherein the alternative DNA marker is a linked marker near MC4R.

31. The method of claim 30 wherein the linked marker is selected from the group consisting of S0331, BHT0433, and S0313.

32. A method of identifying animals which possess a desired genotype indicative of favorable meat quality traits, the method comprising:

determining an association between a MC4R genotype and a trait of interest by obtaining a sample of animals from a line or breed of interest,

preparing a nucleic acid sample from each animal in the sample,

determining the genotype of the MC4R gene, and

calculating the association between the MC4R genotype and the trait.

33. A method of selecting animals which possess a desired MC4R genotype indicative of favorable meat quality traits, the method comprising:

obtaining a nucleic acid sample from an animal,

identifying the genotype of the MC4R gene of the animal, and selecting those animals which have the genotype associated with the desired traits.

34. A method of determining the potential meat quality (value) of an animal, said method comprising:

obtaining a nucleic acid sample from said animal and the
5 assaying for the presence of a polymorphism in the MC4R
 gene of the sample, or a polymorphism linked thereto,
 said polymorphism being one which is associated with
 favorable meat quality characteristics such as pH,
 marbling, color and drip loss.

10 35. A method of selecting animals for breeding, said method
 comprising:

- a) obtaining a nucleic acid sample from said animal;
- 15 b) assaying for the presence of a polymorphism in the
 MC4R gene of said sample or a polymorphism linked
 thereto, said polymorphism being one which is
 associated with favorable meat quality
 characteristics such as pH, marbling, color and
 drop loss; and
- 20 c) using the MC4R genotype as part of a selection
 index based on the estimated value of the effect.

36. A method of segregating animals in order to prove
uniformity at slaughter comprising:

- 25 a) obtaining a nucleic acid sample from said animal;
 and
- b) assaying for the presence of a polymorphism in the
 MC4R gene of said sample or a polymorphism linked
 thereto, said polymorphism being one which is
30 associated with favorable meat quality
 characteristics such as pH, marbling, color and
 drop loss.

37. A method for selecting animals for breeding, said method
35 comprising:

- a) obtaining a nucleic acid sample from said animal;

- b) assaying for the presence of a polymorphism in the MC4R gene of said sample or a polymorphism linked thereto, said polymorphism being one which is associated with favorable meat quality characteristics such as pH, marbling, color and drop loss; and
- c) selecting animals with a favorable allele for inclusion in breeding stock.

10 38. The method of claim 1 wherein said polymorphism is a single nucleotide polymorphism within the MC4R gene or linked to the MC4R gene such that it is associated with variation in meat quality.

15 39. The method claim 1 wherein said polymorphism is a complex polymorphism including repeat link variance (e.g., micro-satellites), insertions or deletions.